

This listing of claims will replace all prior versions and listings of claims in the application:

**Listing of Claims:**

1-18. (Cancelled)

19. (Currently Amended) A method of constructing a library of structurally-constrained peptides comprising

preparing a plurality library of peptides having a scaffold for  $\beta$ -turn display, each peptide comprising a presented turn sequence and a scaffold comprising a first and a second opposite strand[[s]] with a defined backbone hydrogen-bonding pattern, each strand comprising a trpzip domain of at least two Trp residues at non-hydrogen-bonded positions, and each trpzip domain consists of the amino acid sequence WX<sub>1</sub>W, wherein X<sub>1</sub> is independently Thr or independently an amino acid selected from the group consisting of H, V, I, F, Y, and W; and

wherein the Trp residues from each trpzip domain form a cross-strand pair without any disulfide bond, wherein the presented turn sequence is flanked by the first and second opposite strands and comprises random amino acids.

20. (Original) The method of claim 19, wherein the presented turn sequence comprises at least 4 amino acids.

21. (Original) The method of claim 19, wherein the presented turn sequence comprises at least 6 amino acids.

22. (Original) The method of claim 19, wherein each flanking strand consists of naturally occurring L-form amino acids.

23. (Original) The method of claim 19, wherein each flanking strand is at least 3 amino acids in length.

24. (Original) The method of claim 19, wherein each peptide comprises at least 10 amino acids.

25. (Cancelled)

26. (Original) The method of claim 25, wherein each peptide comprises about 12 amino acids.

27. (Original) The method of claim 25, wherein each peptide comprises about 16 amino acids.

28. (Cancelled)

29. (New) The method of claim 19, further comprising contacting the library with a target molecule and isolating peptides that bind to the target molecule.